

Asp Leu Val Ala Val Leu Cys Pro Lys Gly Pro Leu Arg Met Leu Val
 260 265 270
 Glu Thr Ala Gln Glu Arg Asn Glu Thr Leu Phe Pro Ala Leu Ile Tyr
 275 280 285
 Ser Ser Thr Met Val Trp Leu Val Asn Met Ala Glu Gly Asp Pro Glu
 290 295 300
 Ala Gln Arg Arg Val Ser Lys Asn Ser Lys Tyr Asn Ala Glu Ser Thr
 305 310 315 320
 Glu Arg Glu Ser Gln Asp Thr Val Ala Glu Asn Asp Asp Gly Gly Phe
 325 330 335
 Ser Glu Glu Trp Glu Ala Gln Arg Asp Ser His Leu Gly Pro His Arg
 340 345 350
 Ser Thr Pro Glu Ser Arg Ala Ala Val Gln Glu Leu Ser Ser Ser Ile
 355 360 365
 Leu Ala Gly Glu Asp Pro Glu Glu Arg Gly Val Lys Leu Gly Leu Gly
 370 375 380
 Asp Phe Ile Phe Tyr Ser Val Leu Val Gly Lys Ala Ser Ala Thr Ala
 385 390 395 400
 Ser Gly Asp Trp Asn Thr Thr Ile Ala Cys Phe Val Ala Ile Leu Ile
 405 410 415
 Gly Leu Cys Leu Thr Leu Leu Leu Leu Ala Ile Phe Lys Lys Ala Leu
 420 425 430
 Pro Ala Leu Pro Ile Ser Ile Thr Phe Gly Leu Val Phe Tyr Phe Ala
 435 440 445
 Thr Asp Tyr Leu Val Gln Pro Phe Met Asp Gln Leu Ala Phe His Gln
 450 455 460
 Phe Tyr Ile
 465

<210> 2
 <211> 448
 <212> PRT
 <213> human

<400> 2

Met Leu Thr Phe Met Ala Ser Asp Ser Glu Glu Glu Val Cys Asp Glu
 1 5 10 15
 Arg Thr Ser Leu Met Ser Ala Glu Ser Pro Thr Pro Arg Ser Cys Gln
 20 25 30
 Glu Gly Arg Gln Gly Pro Glu Asp Gly Glu Asn Thr Ala Gln Trp Arg
 35 40 45
 Ser Gln Glu Asn Glu Glu Asp Gly Glu Glu Asp Pro Asp Arg Tyr Val
 50 55 60
 Cys Ser Gly Val Pro Gly Arg Pro Pro Gly Leu Glu Glu Glu Leu Thr
 65 70 75 80
 Leu Lys Tyr Gly Ala Lys His Val Ile Met Leu Phe Val Pro Val Thr
 85 90 95
 Leu Cys Met Ile Val Val Val Ala Thr Ile Lys Ser Val Arg Phe Tyr
 100 105 110
 Thr Glu Lys Asn Gly Gln Leu Ile Tyr Thr Pro Phe Thr Glu Asp Thr
 115 120 125
 Pro Ser Val Gly Gln Arg Leu Leu Asn Ser Val Leu Asn Thr Leu Ile
 130 135 140

Met	Ile	Ser	Val	Ile	Val	Val	Met	Thr	Ile	Phe	Leu	Val	Val	Leu	Tyr
145				150						155					160
Lys	Tyr	Arg	Cys	Tyr	Lys	Phe	Ile	His	Gly	Trp	Leu	Ile	Met	Ser	Ser
				165					170					175	
Leu	Met	Leu	Leu	Phe	Leu	Phe	Thr	Tyr	Ile	Tyr	Leu	Gly	Glu	Val	Leu
			180					185					190		
Lys	Thr	Tyr	Asn	Val	Ala	Met	Asp	Tyr	Pro	Thr	Leu	Leu	Leu	Thr	Val
	195						200					205			
Trp	Asn	Phe	Gly	Ala	Val	Gly	Met	Val	Cys	Ile	His	Trp	Lys	Gly	Pro
210						215					220				
Leu	Val	Leu	Gln	Gln	Ala	Tyr	Leu	Ile	Met	Ile	Ser	Ala	Leu	Met	Ala
225					230					235					240
Leu	Val	Phe	Ile	Lys	Tyr	Leu	Pro	Glu	Trp	Ser	Ala	Trp	Val	Ile	Leu
				245					250					255	
Gly	Ala	Ile	Ser	Val	Tyr	Asp	Leu	Val	Ala	Val	Leu	Cys	Pro	Lys	Gly
			260					265					270		
Pro	Leu	Arg	Met	Leu	Val	Glu	Thr	Ala	Gln	Glu	Arg	Asn	Glu	Pro	Ile
		275					280					285			
Phe	Pro	Ala	Leu	Ile	Tyr	Ser	Ser	Ala	Met	Val	Trp	Thr	Val	Gly	Met
	290					295					300				
Ala	Lys	Leu	Asp	Pro	Ser	Ser	Gln	Gly	Ala	Leu	Gln	Leu	Pro	Tyr	Asp
305					310					315					320
Pro	Glu	Met	Glu	Glu	Asp	Ser	Tyr	Asp	Ser	Phe	Gly	Glu	Pro	Ser	Tyr
				325					330					335	
Pro	Glu	Val	Phe	Glu	Pro	Pro	Leu	Thr	Gly	Tyr	Pro	Gly	Glu	Glu	Leu
			340					345					350		
Glu	Glu	Glu	Glu	Glu	Arg	Gly	Val	Lys	Leu	Gly	Leu	Gly	Asp	Phe	Ile
		355					360					365			
Phe	Tyr	Ser	Val	Leu	Val	Gly	Lys	Ala	Ala	Ala	Thr	Gly	Ser	Gly	Asp
	370					375					380				
Trp	Asn	Thr	Thr	Leu	Ala	Cys	Phe	Val	Ala	Ile	Leu	Ile	Gly	Leu	Cys
385					390					395					400
Leu	Thr	Leu	Leu	Leu	Leu	Ala	Val	Phe	Lys	Lys	Ala	Leu	Pro	Ala	Leu
				405					410					415	
Pro	Ile	Ser	Ile	Thr	Phe	Gly	Leu	Ile	Phe	Tyr	Phe	Ser	Thr	Asp	Asn
			420					425					430		
Leu	Val	Arg	Pro	Phe	Met	Asp	Thr	Leu	Ala	Ser	His	Gln	Leu	Tyr	Ile
		435					440					445			

<210> 3
 <211> 4746
 <212> DNA
 <213> human

<400> 3

gccagcatcc	cttgtcccgc	ggccggctca	gacaacaaaa	gcggaagatg	ctgcagttgg	60
gcaaggtcag	gaccttgctt	tgaaagccgg	gcggcgccgc	gcaacgcctc	ttcccggact	120
gaggagctgt	cgccggcgga	gggtgcatgt	ttgcgaggaa	gccgcggggc	gccgcgcctt	180
tgggagctat	gcctgttcca	gaccagcctt	catcagcctc	agagaagacg	agttccctga	240
gccccggctt	aaacacctcc	aacggggatg	gctctgaaac	agaaaccacc	tctgccatcc	300
tcgcctcagt	caaagaacag	gaattacagt	ttgaaaggct	gacccgagag	ctggaggctg	360
aacggcagat	cgtagccagc	cagctggagc	gatgcaagct	cggatccgag	actggcagca	420
tgagcagcat	gagttcagca	gaagagcagt	ttcagtgcca	gtcacaagat	ggtcaaaaag	480

atatcgaaga	tgagcttaca	acaggtctcg	agctgggtgga	ctcctgtatt	aggtcactac	540
aggaatcagg	aatacttgac	ccacaggatt	attctacagg	tgaaaggccc	agcctgctct	600
cccagagtgc	acttcagctc	aattccaaac	ctgaagggtc	tttccagtat	ccggccagct	660
accatagcaa	ccagaccctg	gccctggggg	aaaccacccc	ttcacagctc	ccggcccagag	720
gcacacaagc	ccgagctacg	ggccagagct	tcagccaggg	cacgaccagc	cgcgccggcc	780
acctggcggg	gcccagagccc	gcgcgcgcgc	cgccgcgcgc	gccgcgggag	ccgttcgcgc	840
ccagcctggg	cagcgccttc	cacctgcccg	acgcgcgcgc	cgccgcgcgc	gccgcgcgcgc	900
tctactactc	cagctccacg	ctgcccgcgc	cgccgcgcgc	gggctccccg	ctggccgcgc	960
cccaggggcg	ttcgcccacc	aagctgcagc	gcggcggctc	ggcccccgag	ggcgccacct	1020
acgcgcgcgc	gcgcggctcc	tcgcccgaagc	agtcgcccag	ccgcctggcc	aagtccctaca	1080
gcaccagctc	gcccataaac	atcgctcgtg	cctcgccggg	cctgtccccg	atccgcgtga	1140
cctcgccccc	caccgtgcag	tccaccatct	cctcctcgcc	catccaccag	ctgagctcca	1200
ccatcggcac	gtacgccacc	ctgtcgccca	ccaagcgctt	ggtccacgcg	tccgagcagt	1260
acagcaagca	ctcgcaggag	ctgtatgcca	cggccaccct	ccagaggccg	ggcagcctgg	1320
cagctgggtc	ccgagcctca	tacagcagcc	agcatgggca	cctgggcccc	gagttgcggg	1380
ccctgcagtc	cccagaacac	cacatagatc	ccatctatga	agaccgcgtc	tatcagaagc	1440
cccctatgag	gagtctcagc	cagagccagg	gggacctctt	gccgccagca	cacaccggca	1500
cctaccgcac	gagcacagcc	ccatcttccc	ctgggtgtcg	ctccgtcccc	ttgcagcgca	1560
caggcagcca	gcacggccca	cagaatgccg	ccgcggccac	cttccagagg	gccagctatg	1620
ccgcgggccc	agcctccaat	tacgcggacc	cctaccgaca	gctgcagtat	tgtccctctg	1680
ttgagtctcc	atacagcaaa	tccggccctg	ctctcccgcg	tgaaggcacc	ttggccaggt	1740
ccccgtccat	tgatagcatt	cagaaagatc	ccagagaatt	tggatggaga	gacccggaac	1800
tgccggaagt	gattcagatg	ttgcagcacc	agtttccctc	ggtccagctt	aacgcggcag	1860
ctactttgca	acacctctgt	tttgagagaca	acaaaattaa	agccgagata	aggagacaag	1920
tgaggcatcca	gctcctgggtg	gacctgttgg	atcatcggat	gaccgaagtc	caccgtagtg	1980
ctgtgtggagc	tctgagaaac	ctgggtgtatg	ggaaggccaa	cgatgataac	aaaattgccc	2040
tgaaaaactg	tggtggcattc	ccagcactgg	tgaggttact	ccgcaagacg	actgacctgg	2100
agatccggga	gctggtcaca	ggagtccttt	ggaacctctc	ctcatgcgat	gcactcaaaa	2160
tgccaatcat	ccaggatgcc	ctagcagtag	tgaccaacgc	ggtgattatc	ccccactcag	2220
gctgggaaaa	ttcgctcttt	caggatgatc	ggaaaataca	gctgcattca	tcacaggtgc	2280
tgcgtaacgc	caccgggtgc	ctaaggaatg	ttagttcggc	cggagaggag	gcccgcagaa	2340
ggatgagaga	gtgtgatggg	cttacggatg	ccttgctgta	cgtgatccag	tctgcgctgg	2400
ggagcagtg	gatcgatagc	aagaccgttg	aaaactgtgt	gtgcatttta	aggaacctct	2460
ggtaccggct	ggcggcagaa	acgtctcagg	gacagcacat	gggcacggac	gagctggacg	2520
ggctactctg	tggcgaggcc	aatggcaagg	atgctgagag	ctctgggtgc	tggggcaaga	2580
agaagaagaa	aaagaaatcc	caagatcagt	gggatggagt	aggacctctt	ccagactgtg	2640
ctgaaccacc	aaaagggatc	cagatgctgt	ggcaccatc	aatagtcaaa	ccctacctca	2700
cactgctctc	tgagtgtctc	aatccagaca	cgctggaagg	ggcggcaggc	gccttcgaga	2760
acttggtgc	agggagctgg	aagtgggtcag	tatatatccg	agccgctgtc	cgaaaagaga	2820
aaggcctgcc	catcctcgtg	gagctgctcc	gaatagacaa	tgaccgtgtg	gtgtgcgcgg	2880
tggccactgc	gctgcggaac	atggccttgg	acgtcagaaa	taaggagctc	atcggcaaat	2940
acgccatgcg	agacctagtc	cacaggcttc	caggagggaa	caacagcaac	aacactgcaa	3000
gcaaggccat	gtcggatgac	acagtgcag	ctgtctgctg	cacactgcac	gaagtgatta	3060
ccaagaacat	ggagaacgcc	aaggccttac	gggatgccgg	tggcatcgag	aagttggtcg	3120
gcatctccaa	aagcaaagga	gataaacact	ctccaaaagt	ggtcaaggct	gcatctcagg	3180
tcctcaacag	catgtggcag	taccgagatc	tgaggagtct	ctacaaaaag	gatggatggt	3240
cacaatacca	ctttgtagcc	tcgtcttcaa	ccatcgagag	ggaccggcaa	aggccctact	3300
cctcctcccc	cacgccctcc	atctcccctg	tgcgcgtgtc	tcccaacaac	cgctcagcaa	3360
gtgccccagc	ttcacctcgg	gaaatgatca	gcctcaaaga	aaggaaaaca	gactacgagt	3420
gcaccggcag	caacgccacc	taccacggag	ctaaaggcga	acacacttcc	aggaaagatg	3480
ccatgacagc	tcaaaacact	ggaatttcaa	ctttgtatag	gaattcttat	ggtgcgcccc	3540
ctgaagacat	caaacacaa	caggtttcag	cacagccagt	cccacaggag	cccagcagaa	3600
aagattacga	gacctaccag	ccatttcaga	attccacaag	aaattacgat	gagtccttct	3660

tcgaggacca	ggtccaccat	cgccctccc	ccagcgagta	caccatgcac	ctgggtctca	3720
agtccaccgg	caactacgtt	gacttctact	cagctgccc	tccctacagt	gaactgaact	3780
atgaaacgag	ccactaccgg	gcctcccccg	actcctgggt	gtgaggagca	gggcacaggc	3840
gctccgggaa	cagtgcattg	gcatgcatac	cacaagacat	ttctttctgt	tttgtttttt	3900
tctcctgcaa	atttagtttg	ttaaagcctg	ttccatagga	aggctgtgat	aaccagtaag	3960
gaaatattaa	gagctatttt	agaaagctaa	atgaatcgca	agttaacttg	gaaatcagta	4020
gaaagctaaa	gtgattcctaa	atatgacagt	gggcagcacc	tttctagcgt	gagctgtaaa	4080
gtaacgagaa	gtgctttata	ctgaacgtgg	ttgatgggag	gagagacgag	gcattcgggc	4140
cggtggggcg	taagggttat	cgttaaagcac	aagacacaga	atagtttaca	cactgtgtgg	4200
gggacgggctt	ctcacgcttt	gtttactctc	ttcatccgtt	gtgactctag	gcttcagggt	4260
gcattgggggt	tcctctgtac	agcaagatgt	ttcttgccct	ttgttaatgc	attgttgtaa	4320
agtatttgat	gtacattaca	gattaaagaa	gaaaagcgcg	ttgtgtatat	tacaccaatg	4380
ccgccgtggt	tcctcatcta	tgggttctaaa	tattgcttca	atttcaaact	tttgaaagat	4440
gtatggattt	ccagttttttc	tttactttct	cccagtatgt	tttaacaaaa	aaaaaaaaaaa	4500
gcaggaaaaa	aggaatattt	agcagtattg	ttcgttctga	tatgtgaatt	tgtttgtgac	4560
aactaaacaa	ggcattcagc	agtttctgac	aattaacata	catcattcca	cactccttgt	4620
caacaaagtg	cttttttact	gcctaaaatt	ttagatgtag	atatttgaaa	tagatttttt	4680
catttatacc	agtttttctt	atgatgatac	agtgttaaaa	gaaaataaat	tacaattgat	4740
ctgtca						4746

<210> 4
 <211> 1225
 <212> PRT
 <213> human

<400> 4

Met	Phe	Ala	Arg	Lys	Pro	Pro	Gly	Ala	Ala	Pro	Leu	Gly	Ala	Met	Pro
1				5					10					15	
Val	Pro	Asp	Gln	Pro	Ser	Ser	Ala	Ser	Glu	Lys	Thr	Ser	Ser	Leu	Ser
			20					25					30		
Pro	Gly	Leu	Asn	Thr	Ser	Asn	Gly	Asp	Gly	Ser	Glu	Thr	Glu	Thr	Thr
		35					40					45			
Ser	Ala	Ile	Leu	Ala	Ser	Val	Lys	Glu	Gln	Glu	Leu	Gln	Phe	Glu	Arg
	50					55					60				
Leu	Thr	Arg	Glu	Leu	Glu	Ala	Glu	Arg	Gln	Ile	Val	Ala	Ser	Gln	Leu
65					70				75					80	
Glu	Arg	Cys	Lys	Leu	Gly	Ser	Glu	Thr	Gly	Ser	Met	Ser	Ser	Met	Ser
			85						90					95	
Ser	Ala	Glu	Glu	Gln	Phe	Gln	Trp	Gln	Ser	Gln	Asp	Gly	Gln	Lys	Asp
		100						105					110		
Ile	Glu	Asp	Glu	Leu	Thr	Thr	Gly	Leu	Glu	Leu	Val	Asp	Ser	Cys	Ile
	115						120					125			
Arg	Ser	Leu	Gln	Glu	Ser	Gly	Ile	Leu	Asp	Pro	Gln	Asp	Tyr	Ser	Thr
	130					135					140				
Gly	Glu	Arg	Pro	Ser	Leu	Leu	Ser	Gln	Ser	Ala	Leu	Gln	Leu	Asn	Ser
145					150					155				160	
Lys	Pro	Glu	Gly	Ser	Phe	Gln	Tyr	Pro	Ala	Ser	Tyr	His	Ser	Asn	Gln
			165						170					175	
Thr	Leu	Ala	Leu	Gly	Glu	Thr	Thr	Pro	Ser	Gln	Leu	Pro	Ala	Arg	Gly
		180						185					190		
Thr	Gln	Ala	Arg	Ala	Thr	Gly	Gln	Ser	Phe	Ser	Gln	Gly	Thr	Thr	Ser
	195					200						205			
Arg	Ala	Gly	His	Leu	Ala	Gly	Pro	Glu	Pro	Ala	Pro	Pro	Pro	Pro	Pro

210	215	220
Pro Pro Arg Glu Pro Phe Ala Pro Ser Leu Gly Ser Ala Phe His Leu		
225	230	235
Pro Asp Ala Pro Pro Ala Ala Ala Ala Ala Leu Tyr Tyr Ser Ser		240
	245	250
Ser Thr Leu Pro Ala Pro Pro Arg Gly Gly Ser Pro Leu Ala Ala Pro		255
	260	265
Gln Gly Gly Ser Pro Thr Lys Leu Gln Arg Gly Gly Ser Ala Pro Glu		270
	275	280
Gly Ala Thr Tyr Ala Ala Pro Arg Gly Ser Ser Pro Lys Gln Ser Pro		285
	290	295
Ser Arg Leu Ala Lys Ser Tyr Ser Thr Ser Ser Pro Ile Asn Ile Val		300
305	310	315
Val Ser Ser Ala Gly Leu Ser Pro Ile Arg Val Thr Ser Pro Pro Thr		320
	325	330
Val Gln Ser Thr Ile Ser Ser Ser Pro Ile His Gln Leu Ser Ser Thr		335
	340	345
Ile Gly Thr Tyr Ala Thr Leu Ser Pro Thr Lys Arg Leu Val His Ala		350
	355	360
Ser Glu Gln Tyr Ser Lys His Ser Gln Glu Leu Tyr Ala Thr Ala Thr		365
	370	375
Leu Gln Arg Pro Gly Ser Leu Ala Ala Gly Ser Arg Ala Ser Tyr Ser		380
385	390	395
Ser Gln His Gly His Leu Gly Pro Glu Leu Arg Ala Leu Gln Ser Pro		400
	405	410
Glu His His Ile Asp Pro Ile Tyr Glu Asp Arg Val Tyr Gln Lys Pro		415
	420	425
Pro Met Arg Ser Leu Ser Gln Ser Gln Gly Asp Pro Leu Pro Pro Ala		430
	435	440
His Thr Gly Thr Tyr Arg Thr Ser Thr Ala Pro Ser Ser Pro Gly Val		445
	450	455
Asp Ser Val Pro Leu Gln Arg Thr Gly Ser Gln His Gly Pro Gln Asn		460
465	470	475
Ala Ala Ala Ala Thr Phe Gln Arg Ala Ser Tyr Ala Ala Gly Pro Ala		480
	485	490
Ser Asn Tyr Ala Asp Pro Tyr Arg Gln Leu Gln Tyr Cys Pro Ser Val		495
	500	505
Glu Ser Pro Tyr Ser Lys Ser Gly Pro Ala Leu Pro Pro Glu Gly Thr		510
	515	520
Leu Ala Arg Ser Pro Ser Ile Asp Ser Ile Gln Lys Asp Pro Arg Glu		525
	530	535
Phe Gly Trp Arg Asp Pro Glu Leu Pro Glu Val Ile Gln Met Leu Gln		540
545	550	555
His Gln Phe Pro Ser Val Gln Ser Asn Ala Ala Ala Tyr Leu Gln His		560
	565	570
Leu Cys Phe Gly Asp Asn Lys Ile Lys Ala Glu Ile Arg Arg Gln Gly		575
	580	585
Gly Ile Gln Leu Leu Val Asp Leu Leu Asp His Arg Met Thr Glu Val		590
	595	600
His Arg Ser Ala Cys Gly Ala Leu Arg Asn Leu Val Tyr Gly Lys Ala		605
	610	620
Asn Asp Asp Asn Lys Ile Ala Leu Lys Asn Cys Gly Gly Ile Pro Ala		630
625	630	635
		640

Leu	Val	Arg	Leu	Leu	Arg	Lys	Thr	Thr	Asp	Leu	Glu	Ile	Arg	Glu	Leu
				645					650					655	
Val	Thr	Gly	Val	Leu	Trp	Asn	Leu	Ser	Ser	Cys	Asp	Ala	Leu	Lys	Met
			660					665					670		
Pro	Ile	Ile	Gln	Asp	Ala	Leu	Ala	Val	Leu	Thr	Asn	Ala	Val	Ile	Ile
		675					680					685			
Pro	His	Ser	Gly	Trp	Glu	Asn	Ser	Pro	Leu	Gln	Asp	Asp	Arg	Lys	Ile
	690					695					700				
Gln	Leu	His	Ser	Ser	Gln	Val	Leu	Arg	Asn	Ala	Thr	Gly	Cys	Leu	Arg
705					710					715					720
Asn	Val	Ser	Ser	Ala	Gly	Glu	Glu	Ala	Arg	Arg	Arg	Met	Arg	Glu	Cys
				725					730					735	
Asp	Gly	Leu	Thr	Asp	Ala	Leu	Leu	Tyr	Val	Ile	Gln	Ser	Ala	Leu	Gly
			740					745					750		
Ser	Ser	Glu	Ile	Asp	Ser	Lys	Thr	Val	Glu	Asn	Cys	Val	Cys	Ile	Leu
		755					760					765			
Arg	Asn	Leu	Ser	Tyr	Arg	Leu	Ala	Ala	Glu	Thr	Ser	Gln	Gly	Gln	His
	770					775					780				
Met	Gly	Thr	Asp	Glu	Leu	Asp	Gly	Leu	Leu	Cys	Gly	Glu	Ala	Asn	Gly
785					790					795					800
Lys	Asp	Ala	Glu	Ser	Ser	Gly	Cys	Trp	Gly	Lys	Lys	Lys	Lys	Lys	Lys
				805					810					815	
Lys	Ser	Gln	Asp	Gln	Trp	Asp	Gly	Val	Gly	Pro	Leu	Pro	Asp	Cys	Ala
			820					825					830		
Glu	Pro	Pro	Lys	Gly	Ile	Gln	Met	Leu	Trp	His	Pro	Ser	Ile	Val	Lys
		835					840					845			
Pro	Tyr	Leu	Thr	Leu	Leu	Ser	Glu	Cys	Ser	Asn	Pro	Asp	Thr	Leu	Glu
	850					855					860				
Gly	Ala	Ala	Gly	Ala	Leu	Gln	Asn	Leu	Ala	Ala	Gly	Ser	Trp	Lys	Trp
865					870					875					880
Ser	Val	Tyr	Ile	Arg	Ala	Ala	Val	Arg	Lys	Glu	Lys	Gly	Leu	Pro	Ile
				885					890					895	
Leu	Val	Glu	Leu	Leu	Arg	Ile	Asp	Asn	Asp	Arg	Val	Val	Cys	Ala	Val
		900						905					910		
Ala	Thr	Ala	Leu	Arg	Asn	Met	Ala	Leu	Asp	Val	Arg	Asn	Lys	Glu	Leu
		915					920					925			
Ile	Gly	Lys	Tyr	Ala	Met	Arg	Asp	Leu	Val	His	Arg	Leu	Pro	Gly	Gly
	930					935					940				
Asn	Asn	Ser	Asn	Asn	Thr	Ala	Ser	Lys	Ala	Met	Ser	Asp	Asp	Thr	Val
945					950					955					960
Thr	Ala	Val	Cys	Cys	Thr	Leu	His	Glu	Val	Ile	Thr	Lys	Asn	Met	Glu
				965					970					975	
Asn	Ala	Lys	Ala	Leu	Arg	Asp	Ala	Gly	Gly	Ile	Glu	Lys	Leu	Val	Gly
			980					985					990		
Ile	Ser	Lys	Ser	Lys	Gly	Asp	Lys	His	Ser	Pro	Lys	Val	Val	Lys	Ala
		995					1000					1005			
Ala	Ser	Gln	Val	Leu	Asn	Ser	Met	Trp	Gln	Tyr	Arg	Asp	Leu	Arg	Ser
		1010					1015				1020				
Leu	Tyr	Lys	Lys	Asp	Gly	Trp	Ser	Gln	Tyr	His	Phe	Val	Ala	Ser	Ser
1025					1030					1035					104
Ser	Thr	Ile	Glu	Arg	Asp	Arg	Gln	Arg	Pro	Tyr	Ser	Ser	Ser	Arg	Thr
				1045					1050					1055	
Pro	Ser	Ile	Ser	Pro	Val	Arg	Val	Ser	Pro	Asn	Asn	Arg	Ser	Ala	Ser

1060	1065	1070
Ala Pro Ala Ser Pro Arg Glu Met Ile Ser Leu Lys Glu Arg Lys Thr		
1075	1080	1085
Asp Tyr Glu Cys Thr Gly Ser Asn Ala Thr Tyr His Gly Ala Lys Gly		
1090	1095	1100
Glu His Thr Ser Arg Lys Asp Ala Met Thr Ala Gln Asn Thr Gly Ile		
1105	1110	1115
Ser Thr Leu Tyr Arg Asn Ser Tyr Gly Ala Pro Ala Glu Asp Ile Lys		
1125	1130	1135
His Asn Gln Val Ser Ala Gln Pro Val Pro Gln Glu Pro Ser Arg Lys		
1140	1145	1150
Asp Tyr Glu Thr Tyr Gln Pro Phe Gln Asn Ser Thr Arg Asn Tyr Asp		
1155	1160	1165
Glu Ser Phe Phe Glu Asp Gln Val His His Arg Pro Pro Ala Ser Glu		
1170	1175	1180
Tyr Thr Met His Leu Gly Leu Lys Ser Thr Gly Asn Tyr Val Asp Phe		
1185	1190	1195
Tyr Ser Ala Ala Arg Pro Tyr Ser Glu Leu Asn Tyr Glu Thr Ser His		
1205	1210	1215
Tyr Pro Ala Ser Pro Asp Ser Trp Val		
1220	1225	

<210> 5
 <211> 4998
 <212> DNA
 <213> mouse

<400> 5

agcgccgga	gccggccgcc	gcggctgagc	cggaggctga	gctgcggcgc	gcggcgggag	60
gagcctcgct	ctcggcgggc	gcggcggcgc	cggcgacaca	ggtggcgcg	gcggcgcgca	120
gggcgagct	cgagagcgct	cggcgccggg	cgccaggcg	gcccaggctc	gcgcccgcgg	180
gggcaaccgg	ccgagcggag	cggcgggcgc	ggcggtcgg	tagcccggcc	cgagcccggg	240
gagccccgcg	gaaccctgag	catcccgcgg	cgcccgcga	gtcgggcagg	gggcgctacg	300
ctcgccgcgc	tcggaggggc	ggccggggcc	ggcgctgcgc	actcgcgtcg	ggagccgcct	360
ctcgctgcc	gcgctcgccc	ctgctccccg	ccagcatcac	ttgtcccgcg	gccgcgctcc	420
gacaacaaaa	gcggaggatg	ctgcagctgg	gcaaggtcag	gaccttgctc	tgaagccggg	480
cgggcggcgc	cacgcctttc	ccccgactga	ggagctgtct	ttggcgggcg	gtgcatgttc	540
gccaggaagc	agtcgggcgc	cgcgccttcc	ggagctatgc	ctgtcccaga	ccagcctcca	600
tcagcctcag	agaagaacag	ctccttgagc	ccaggcttaa	acacctccaa	tggtgatggc	660
tctgagacgg	aaaccacctc	tgctatcctt	gcctccgtca	aagaacagga	attacagttt	720
gaaaggctga	cccagagagc	ggaggctgaa	cgccagatcg	tagccagcca	gctggagcga	780
tgcaagcttg	gctcggagac	aggaagcatg	agcagtatca	gttcagcagg	agagcagttt	840
cactggcaga	cacaagatgg	ccaaaaagat	atcgaagatg	aacttacaac	gggccttgag	900
ctggtggact	cctgtatccg	ctctctgcag	gagtcaggca	ttctggaccc	acaggattac	960
tccacaagtg	aaaggcctag	cctgctctcc	cagagtgcac	ttcagctcaa	ttctaaacct	1020
gaagggctct	tccagtatcc	ggccagctac	catagcaacc	agaccctggc	cctgggtgac	1080
acagcccctt	ctcagctccc	agcacgcagc	acgcaagccc	gagctgccgg	ccagagcttc	1140
agccagggca	cgaccggccg	cgcggggcac	ctggcgggct	ccgagcctgc	gccaccgcct	1200
ccgcctccgc	gggaaccgtt	cgcgcccagc	ctgggcagcg	ccttccacct	gcccgcgcgc	1260
ccgcccgcgc	ccgcggcgct	ctactactcc	agctccacgc	tgcccgcgcc	gccgcgcggg	1320
ggctccccgc	tgaccaccac	gcagggcggc	tcacccacca	agctgcagcg	cggaggctcg	1380
gcccccgagg	gtgccgccta	cgcgcgcgcg	cgcggctcct	cgcccaagca	gtcgcgccagc	1440
cgctgggcta	agtcctacag	caccagctcg	cccatcaaca	tcgtcgtgtc	ctcggccggc	1500

ctgtccccga	tccgcgtgac	ctcgcccccc	accgtgcagt	ccaccatctc	ctcttcgccc	1560
atccaccagc	tgagctccac	catcggcacc	tacgccaccc	tgtcgccac	caagcgctg	1620
gtccacgcgt	ctgagcagta	cagcaagcat	tcgaggagc	tgtatgccac	cgccaccctc	1680
cagaggccgg	gcagcctggc	agctggatcc	cgagcctcgt	atagcagcca	gcattgggac	1740
ctggcccttg	agctgcgggc	cctgcagtcc	ccagagcacc	acatagaccc	catctatgaa	1800
gaccgtgtct	atcagaagcc	ccctatgagg	agtctcagcc	agagccaggg	ggatcctctg	1860
ccgccagcac	ataccggcac	cttcgcacg	agcacagccc	cgtcctcccc	tgggtgcgac	1920
tccgtccctt	tgcagcgcac	aggcagccaa	cacgggccac	agaatgccgc	cgcagccacc	1980
ttccagaggg	ccagctatgc	tgcgggcccc	gcctccaact	acgcagaccc	ctaccgacag	2040
ctgcagtatt	gtgcctccgt	tgactctccg	tacagcaaact	ctggccctgc	cctcccaccc	2100
gaaggcacct	tggccagatc	cccatccatc	gacagcattc	agaaagaccc	cagggagttt	2160
ggatggagag	acccggagct	gcctgaagtg	atacagatgt	tacagcacca	gttcccttca	2220
gtccagtcga	atgctgcagc	ttacctgcaa	cacctctgtt	ttggagacaa	taaaattaag	2280
gcagagataa	ggagacaagg	agggatacag	ctcctggtgg	acctgctgga	tcaccgaatg	2340
acagaagtcc	accgtagtgc	ctgtggggct	ctgaggaacc	tgggtgatgg	gaaggccaat	2400
gatgataaca	aaatcgccct	gaaaaactgt	ggtggtatcc	cagcgtctgg	gagactcctt	2460
cgcaagacca	cagacctgga	gatccgggag	ctggtcacag	gagtcctttg	gaacctctca	2520
tcattgtgat	cactcaaaat	gccaatcatc	caggacgccc	tggcagtgtc	gaccaatgcy	2580
gtgattatcc	ctcactcggg	ctgggagaat	tcacctcttc	aggatgatcg	gaaaatacag	2640
ctgcattcat	cacaggtgct	gcgcaacgcc	actgggtgcc	taaggaaatg	aagttcagct	2700
ggagaggagg	cccgcgaag	gatgcgggag	tgtgatgggc	tcacggatgc	cttgcctgtac	2760
gtgatccagt	ctgcactggg	gagcagtggg	atcgatagca	agaccgttga	aaactgtgtg	2820
tgcatcttga	ggaacctctc	ctaccggcta	gcagcagaaa	cgtctcaggg	acagcacatg	2880
ggcacagacg	agctggacgg	gctgctctgc	ggggagacca	acggcaaaga	cacagagagt	2940
ctctgggtgct	ggggcaagaa	gaagaagaaa	aagaaatccc	aggaccagtg	ggatggagta	3000
ggacctcttc	cagactgtgc	agagccacca	aaagggatcc	agatgctgtg	gcaccctgct	3060
atagtcaaac	cctacctcac	actgctctct	gagtgtctaa	accagacac	gctggaaggg	3120
gcagcggggc	ccctgcagaa	cttggctgca	gggagctgga	agggctgggc	tgaggatgtg	3180
gcaggcatgg	cgtatgccct	acgttactct	ccagaggggg	ctccctgcct	gccacagtgg	3240
tcctgtgtata	tccgagctgc	tgtccggaaa	gagaaaggcc	tgcccattct	tgtggagctc	3300
ctccgaatat	acaatgaccg	tgtagtgtgt	gcagtggcca	cagcacttcg	gaacatggcc	3360
ctcgatgtca	gaaacaagga	actcattggc	aagtatgcca	tgcgagacct	ggtccaccgg	3420
cttccctggg	ggaacaacag	caacaactcg	gggagcaagg	ccatgtcaga	tgacaccgtg	3480
acggccctgt	gctgcacctc	gcattgaagt	atcaccaaga	acatggagaa	tgccaaggcc	3540
ttacgggatg	ctgggtggcat	cgagaagttg	gtcggcatct	ctaaaagcaa	aggagacaag	3600
cactctccaa	aggtggtcaa	ggctgcttct	caggtcctaa	acagcatgtg	gcagtatcgc	3660
gatctgagga	gtctctacaa	gaaggatgga	tggtcacaat	atcactttgt	agcctcatct	3720
tcaaccatcg	agagggatcg	acaaaggccc	tactcctcct	cccgacaccc	ctccatctct	3780
cccggtgcgtg	tgtctcccaa	caaccgctca	gcaagtgcct	cagcttcacc	tcgggaaatg	3840
atcagcctca	aagaaaggaa	gacggactac	gagtcgctg	gcaacaacgc	cacttaccac	3900
ggaactaaag	gagaacacac	ctccagaaaa	gacaccatga	cagctcaaaa	cactggagtt	3960
tcaactttgt	acaggaattc	atacgggtcg	cccgtgaag	acatcaaaca	gaaccaggtt	4020
tccacacagc	ctgtccctca	ggagcccagc	aggaaagact	acgagacctc	ccagcccttt	4080
ccgaattcca	cacgaaatta	tgatgagtc	ttctttgagg	accaggtcca	ccaccgcctt	4140
ccagccagcg	agtacaccat	gcacctgggc	ctcaagtcca	ctggcaacta	tgtcgacttc	4200
tactctgcag	cccgctcctta	cagtgaactg	aactatgaaa	cgagccacta	cccggcctcg	4260
cccgaactcct	gggtgtaagg	agccaggaca	cgaggcactc	cggggacagt	gcattgtgcat	4320
gcatacacca	caggacattt	tgtttctttt	tttcttttct	tttcttttgt	tttttttttt	4380
ttttctttcc	ctgcaaattt	agtttggttaa	agcctgttcc	gtaggaaggc	tgtgataacc	4440
aggaagaaat	actcagagct	atttttagaaa	gctaaaatga	atcaagagtt	aactgggaaa	4500
tcgataggaa	gctaaacgca	atcctaattg	tgaccgcatt	caacaccttt	ctagtttgaa	4560
ctatagcatt	ttgaaagtgc	tttatagtc	ggtgaggctg	aaggtaggag	agaggagaca	4620
gtcagggtgg	tgggcgtggt	tatcgctaag	cacaagacag	actagtttac	acactgtggg	4680

gacggcttct	cacgctttgt	ttactctctt	catccgtgtg	actctaggct	tcaagttgca	4740
ttgggggttc	tctgtacagc	aagacgtctc	ttgccttttg	ttaatgcatt	gttgtaaagt	4800
attcgatgta	cattacagat	taaagacgaa	gagtgcatgg	tgtatattac	accaatgcc	4860
ctgtgtttcc	tcatcaatgg	ttctaaatat	tgcttcaatt	tcaaactttt	gaaagatgta	4920
tgggtttcca	attttctttt	tttttttctt	tctcccagta	tgttttaaca	aaaaaggaaa	4980
aaaaaacag	gaaaaaaa					4998

<210> 6
 <211> 1247
 <212> PRT
 <213> mouse

<400> 6

Met	Phe	Ala	Arg	Lys	Gln	Ser	Gly	Ala	Ala	Pro	Phe	Gly	Ala	Met	Pro
1				5					10					15	
Val	Pro	Asp	Gln	Pro	Pro	Ser	Ala	Ser	Glu	Lys	Asn	Ser	Ser	Leu	Ser
			20					25					30		
Pro	Gly	Leu	Asn	Thr	Ser	Asn	Gly	Asp	Gly	Ser	Glu	Thr	Glu	Thr	Thr
		35					40					45			
Ser	Ala	Ile	Leu	Ala	Ser	Val	Lys	Glu	Gln	Glu	Leu	Gln	Phe	Glu	Arg
	50					55					60				
Leu	Thr	Arg	Glu	Leu	Glu	Ala	Glu	Arg	Gln	Ile	Val	Ala	Ser	Gln	Leu
65				70					75					80	
Glu	Arg	Cys	Lys	Leu	Gly	Ser	Glu	Thr	Gly	Ser	Met	Ser	Ser	Ile	Ser
			85						90					95	
Ser	Ala	Gly	Glu	Gln	Phe	His	Trp	Gln	Thr	Gln	Asp	Gly	Gln	Lys	Asp
			100					105					110		
Ile	Glu	Asp	Glu	Leu	Thr	Thr	Gly	Leu	Glu	Leu	Val	Asp	Ser	Cys	Ile
	115						120					125			
Arg	Ser	Leu	Gln	Glu	Ser	Gly	Ile	Leu	Asp	Pro	Gln	Asp	Tyr	Ser	Thr
	130					135					140				
Ser	Glu	Arg	Pro	Ser	Leu	Leu	Ser	Gln	Ser	Ala	Leu	Gln	Leu	Asn	Ser
145				150						155				160	
Lys	Pro	Glu	Gly	Ser	Phe	Gln	Tyr	Pro	Ala	Ser	Tyr	His	Ser	Asn	Gln
			165						170					175	
Thr	Leu	Ala	Leu	Gly	Asp	Thr	Ala	Pro	Ser	Gln	Leu	Pro	Ala	Arg	Ser
		180						185					190		
Thr	Gln	Ala	Arg	Ala	Ala	Gly	Gln	Ser	Phe	Ser	Gln	Gly	Thr	Thr	Gly
	195					200						205			
Arg	Ala	Gly	His	Leu	Ala	Gly	Ser	Glu	Pro	Ala	Pro	Pro	Pro	Pro	Pro
	210					215					220				
Pro	Arg	Glu	Pro	Phe	Ala	Pro	Ser	Leu	Gly	Ser	Ala	Phe	His	Leu	Pro
225				230						235				240	
Asp	Ala	Pro	Pro	Ala	Ala	Ala	Ala	Leu	Tyr	Tyr	Ser	Ser	Ser	Thr	Leu
			245					250						255	
Pro	Ala	Pro	Pro	Arg	Gly	Gly	Ser	Pro	Leu	Thr	Thr	Thr	Gln	Gly	Gly
		260					265						270		
Ser	Pro	Thr	Lys	Leu	Gln	Arg	Gly	Gly	Ser	Ala	Pro	Glu	Gly	Ala	Ala
	275					280					285				
Tyr	Ala	Ala	Pro	Arg	Gly	Ser	Ser	Pro	Lys	Gln	Ser	Pro	Ser	Arg	Leu
	290				295						300				
Ala	Lys	Ser	Tyr	Ser	Thr	Ser	Ser	Pro	Ile	Asn	Ile	Val	Val	Ser	Ser
305					310					315					320

Ala	Gly	Leu	Ser	Pro	Ile	Arg	Val	Thr	Ser	Pro	Pro	Thr	Val	Gln	Ser	325	330	335
Thr	Ile	Ser	Ser	Ser	Pro	Ile	His	Gln	Leu	Ser	Ser	Thr	Ile	Gly	Thr	340	345	350
Tyr	Ala	Thr	Leu	Ser	Pro	Thr	Lys	Arg	Leu	Val	His	Ala	Ser	Glu	Gln	355	360	365
Tyr	Ser	Lys	His	Ser	Gln	Glu	Leu	Tyr	Ala	Thr	Ala	Thr	Leu	Gln	Arg	370	375	380
Pro	Gly	Ser	Leu	Ala	Ala	Gly	Ser	Arg	Ala	Ser	Tyr	Ser	Ser	Gln	His	385	390	395
Gly	His	Leu	Ala	Pro	Glu	Leu	Arg	Ala	Leu	Gln	Ser	Pro	Glu	His	His	405	410	415
Ile	Asp	Pro	Ile	Tyr	Glu	Asp	Arg	Val	Tyr	Gln	Lys	Pro	Pro	Met	Arg	420	425	430
Ser	Leu	Ser	Gln	Ser	Gln	Gly	Asp	Pro	Leu	Pro	Pro	Ala	His	Thr	Gly	435	440	445
Thr	Phe	Arg	Thr	Ser	Thr	Ala	Pro	Ser	Ser	Pro	Gly	Val	Asp	Ser	Val	450	455	460
Pro	Leu	Gln	Arg	Thr	Gly	Ser	Gln	His	Gly	Pro	Gln	Asn	Ala	Ala	Ala	465	470	475
Ala	Thr	Phe	Gln	Arg	Ala	Ser	Tyr	Ala	Ala	Gly	Pro	Ala	Ser	Asn	Tyr	485	490	495
Ala	Asp	Pro	Tyr	Arg	Gln	Leu	Gln	Tyr	Cys	Ala	Ser	Val	Asp	Ser	Pro	500	505	510
Tyr	Ser	Lys	Ser	Gly	Pro	Ala	Leu	Pro	Pro	Glu	Gly	Thr	Leu	Ala	Arg	515	520	525
Ser	Pro	Ser	Ile	Asp	Ser	Ile	Gln	Lys	Asp	Pro	Arg	Glu	Phe	Gly	Trp	530	535	540
Arg	Asp	Pro	Glu	Leu	Pro	Glu	Val	Ile	Gln	Met	Leu	Gln	His	Gln	Phe	545	550	555
Pro	Ser	Val	Gln	Ser	Asn	Ala	Ala	Ala	Tyr	Leu	Gln	His	Leu	Cys	Phe	565	570	575
Gly	Asp	Asn	Lys	Ile	Lys	Ala	Glu	Ile	Arg	Arg	Gln	Gly	Gly	Ile	Gln	580	585	590
Leu	Leu	Val	Asp	Leu	Leu	Asp	His	Arg	Met	Thr	Glu	Val	His	Arg	Ser	595	600	605
Ala	Cys	Gly	Ala	Leu	Arg	Asn	Leu	Val	Tyr	Gly	Lys	Ala	Asn	Asp	Asp	610	615	620
Asn	Lys	Ile	Ala	Leu	Lys	Asn	Cys	Gly	Gly	Ile	Pro	Ala	Leu	Val	Arg	625	630	635
Leu	Leu	Arg	Lys	Thr	Thr	Asp	Leu	Glu	Ile	Arg	Glu	Leu	Val	Thr	Gly	645	650	655
Val	Leu	Trp	Asn	Leu	Ser	Ser	Cys	Asp	Ala	Leu	Lys	Met	Pro	Ile	Ile	660	665	670
Gln	Asp	Ala	Leu	Ala	Val	Leu	Thr	Asn	Ala	Val	Ile	Ile	Pro	His	Ser	675	680	685
Gly	Trp	Glu	Asn	Ser	Pro	Leu	Gln	Asp	Asp	Arg	Lys	Ile	Gln	Leu	His	690	695	700
Ser	Ser	Gln	Val	Leu	Arg	Asn	Ala	Thr	Gly	Cys	Leu	Arg	Asn	Val	Ser	705	710	715
Ser	Ala	Gly	Glu	Glu	Ala	Arg	Arg	Arg	Met	Arg	Glu	Cys	Asp	Gly	Leu	725	730	735
Thr	Asp	Ala	Leu	Leu	Tyr	Val	Ile	Gln	Ser	Ala	Leu	Gly	Ser	Ser	Glu			

			740					745					750				
Ile	Asp	Ser	Lys	Thr	Val	Glu	Asn	Cys	Val	Cys	Ile	Leu	Arg	Asn	Leu		
		755					760					765					
Ser	Tyr	Arg	Leu	Ala	Ala	Glu	Thr	Ser	Gln	Gly	Gln	His	Met	Gly	Thr		
	770					775					780						
Asp	Glu	Leu	Asp	Gly	Leu	Leu	Cys	Gly	Glu	Thr	Asn	Gly	Lys	Asp	Thr		
785					790					795					800		
Glu	Ser	Ser	Gly	Cys	Trp	Gly	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Ser	Gln		
			805					810						815			
Asp	Gln	Trp	Asp	Gly	Val	Gly	Pro	Leu	Pro	Asp	Cys	Ala	Glu	Pro	Pro		
			820					825					830				
Lys	Gly	Ile	Gln	Met	Leu	Trp	His	Pro	Ser	Ile	Val	Lys	Pro	Tyr	Leu		
	835						840					845					
Thr	Leu	Leu	Ser	Glu	Cys	Ser	Asn	Pro	Asp	Thr	Leu	Glu	Gly	Ala	Ala		
	850					855					860						
Gly	Ala	Leu	Gln	Asn	Leu	Ala	Ala	Gly	Ser	Trp	Lys	Gly	Trp	Ala	Glu		
865					870					875					880		
Asp	Val	Ala	Gly	Met	Ala	Tyr	Ala	Leu	Arg	Ser	Leu	Pro	Glu	Gly	Ala		
			885					890						895			
Pro	Cys	Leu	Pro	Gln	Trp	Ser	Val	Tyr	Ile	Arg	Ala	Ala	Val	Arg	Lys		
			900					905					910				
Glu	Lys	Gly	Leu	Pro	Ile	Leu	Val	Glu	Leu	Leu	Arg	Ile	Asp	Asn	Asp		
	915						920					925					
Arg	Val	Val	Cys	Ala	Val	Ala	Thr	Ala	Leu	Arg	Asn	Met	Ala	Leu	Asp		
	930					935					940						
Val	Arg	Asn	Lys	Glu	Leu	Ile	Gly	Lys	Tyr	Ala	Met	Arg	Asp	Leu	Val		
945					950					955					960		
His	Arg	Leu	Pro	Gly	Gly	Asn	Asn	Ser	Asn	Asn	Ser	Gly	Ser	Lys	Ala		
			965					970						975			
Met	Ser	Asp	Asp	Thr	Val	Thr	Ala	Val	Cys	Cys	Thr	Leu	His	Glu	Val		
		980						985					990				
Ile	Thr	Lys	Asn	Met	Glu	Asn	Ala	Lys	Ala	Leu	Arg	Asp	Ala	Gly	Gly		
	995						1000					1005					
Ile	Glu	Lys	Leu	Val	Gly	Ile	Ser	Lys	Ser	Lys	Gly	Asp	Lys	His	Ser		
	1010					1015					1020						
Pro	Lys	Val	Val	Lys	Ala	Ala	Ser	Gln	Val	Leu	Asn	Ser	Met	Trp	Gln		
1025					1030					1035					104		
Tyr	Arg	Asp	Leu	Arg	Ser	Leu	Tyr	Lys	Lys	Asp	Gly	Trp	Ser	Gln	Tyr		
			1045					1050						1055			
His	Phe	Val	Ala	Ser	Ser	Ser	Thr	Ile	Glu	Arg	Asp	Arg	Gln	Arg	Pro		
		1060						1065					1070				
Tyr	Ser	Ser	Ser	Arg	Thr	Pro	Ser	Ile	Ser	Pro	Val	Arg	Val	Ser	Pro		
	1075						1080					1085					
Asn	Asn	Arg	Ser	Ala	Ser	Ala	Pro	Ala	Ser	Pro	Arg	Glu	Met	Ile	Ser		
	1090					1095					1100						
Leu	Lys	Glu	Arg	Lys	Thr	Asp	Tyr	Glu	Ser	Ala	Gly	Asn	Asn	Ala	Thr		
1105					1110					1115					112		
Tyr	His	Gly	Thr	Lys	Gly	Glu	His	Thr	Ser	Arg	Lys	Asp	Thr	Met	Thr		
			1125					1130						1135			
Ala	Gln	Asn	Thr	Gly	Val	Ser	Thr	Leu	Tyr	Arg	Asn	Ser	Tyr	Gly	Ala		
		1140						1145					1150				
Pro	Ala	Glu	Asp	Ile	Lys	Gln	Asn	Gln	Val	Ser	Thr	Gln	Pro	Val	Pro		
	1155						1160						1165				

